We claim:

1. A drug delivery system comprising:

a polymeric encapsulation medium made by self-assembly of a plurality of polypeptides; and

at least one drug encapsulated in said polymeric encapsulation medium.

2. The drug delivery system as claimed in claim 1 further comprising a targeting vector.

3. The drug delivery system as claimed in claim 1, wherein each of the plurality of has at least 50% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

4. The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides has at least 60% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

5. The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides has at least 70% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

6. The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides has at least 80% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

7. The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides has at least 90% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

8. The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides has at least 95% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

9. The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides comprises at least 10 consecutive amino acids of a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

10. The drug delivery system as claimed in claim 9, wherein each of the plurality of polypeptides has at least 50% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

11. The drug delivery system as claimed in claim 9, wherein each of the plurality of polypeptides has at least 60% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

12. The drug delivery system as claimed in claim 9, wherein each of the plurality of polypeptides has at least 70% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

13. The drug delivery system as claimed in claim 9, wherein each of the plurality of polypeptides has at least 80% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

14. The drug delivery system as claimed in claim 9, wherein each of the plurality of polypeptides has at least 90% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

15. The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides is encoded by a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency.

16. The drug delivery system as claimed in claim 15, wherein each of the plurality of polypeptides is encoded by a first nucleic acid, which hybridizes to a second nucleic acid under conditions of high stringency.

17. The drug delivery system as claimed in claim 15, wherein each of the plurality of polypeptides is encoded by a first nucleic acid, which hybridizes to a second nucleic acid under conditions of moderate stringency.

18. The drug delivery system as claimed in claim 15, wherein each of the plurality of polypeptides is encoded by a first nucleic acid, which hybridizes to a second nucleic acid under conditions of low stringency.

19. The drug delivery system as claimed in claim 15, wherein said variants have at least about 50% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 200 residues..

20. The drug delivery system as claimed in claim 15, wherein the nucleic acid comprises a sequence having at least 50% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9 over the entire sequence.

21. The drug delivery system as claimed in claim 15, wherein the nucleic acid comprises a sequence having at least 60% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9 over the entire sequence.

22. The drug delivery system as claimed in claim 15, wherein the nucleic acid comprises a sequence having at least 70% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9 over the entire sequence..

23. The drug delivery system as claimed in claim 15, wherein the nucleic acid comprises a sequence having at least 80% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9 over the entire sequence.

24. The drug delivery system as claimed in claim 15, wherein the nucleic acid comprises a sequence having at least 90% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9 over the entire sequence.

25. The drug delivery system as claimed in claim 15, wherein the nucleic acid comprises a sequence selected from the group consisting of SEQ ID NOS: I, 3, 5, 7, 9.

26. The drug delivery system as claimed in claim 15, wherein the nucleic acid comprises at least 10 consecutive bases of a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency.

27. The drug delivery system as claimed in claim 26, wherein the nucleic acid comprises a sequence having at least 60% homology to the nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9.

28. The drug delivery system as claimed in claim 26, wherein the nucleic acid comprises a sequence having at least 70% homology to the nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9.

29. The drug delivery system as claimed in claim 26, wherein the nucleic acid comprises a sequence having at least 80% homology to the nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9.

30. The drug delivery system as claimed in claim 26, wherein the nucleic acid comprises a sequence having at least 90% homology to the nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9.

31. A method of producing a polypeptide polymer by self-assembly comprising the steps of:

providing a plurality of polypeptides capable of self-assembly in the presence of a divalent cation; and

polymerizing the polypeptides in the presence of a divalent cation and a template molecule.

32. A method as claimed in claim 31, wherein the polypeptide has a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, and sequences having at least 50% homology to a sequence selected from SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

33. A method as claimed in claim 31, wherein the polypeptide is encoded by a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency.

34. The method as claimed in claim 31, wherein the step of providing a plurality of polypeptides further comprises the steps of:

preparing a vector with a nucleic acid attached, wherein the nucleic acid encodes the polypeptide;

inserting the vector into a host cell;

growing the host cell in a suitable culture to express the nucleic acid to form the polypeptide; and

isolating the formed polypeptide from the host cell.

35. The method as claimed in claim 31, wherein the step of polymerizing the polypeptides further comprises the steps of:

dissolving the plurality of polypeptides in a solution; and

adding a template molecule and alkaline earth metal ions to the solution.

36. The method as claimed in claim 34, wherein the vector comprises plasmid pEX-CAN-A.

37. The method as claimed in claim 36, wherein the host cell comprises a host cell selected from the group consisting of E. Coli BL21 (DE3) and pseudomonas.

38. A method of delivering a drug to a location in the human or animal body comprising the step of:

administering a drug delivery system as claimed in claim 1 to a human or animal body.

39. The method as claimed in claim 38, further comprising the step of releasing the drug from the delivery system at the location in the human or animal body.

40. The method as claimed in claim 38, further comprising the steps of:

dissolving the plurality of polypeptides and the drug in a solution; and

polymerizing the plurality of polypeptides in the presence of the drug so as to encapsulate the drug in the polymer to form the drug delivery system.

41. A method of encapsulating a molecule comprising the steps of:

providing a solution of a plurality of polypeptides having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, and sequences having at least 50% homology to a sequence selected from SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection; and

polymerizing the plurality of polypeptides the presence of the molecule so as to encapsulate the molecule in the polymer.

42. The method as claimed in claim 41, wherein at least one of said polypeptides comprises a target vector.

43. A method of encapsulating a molecule comprising the steps of:

providing a solution of a plurality of polypeptides, wherein each polypeptide is encoded by a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency; and

polymerizing the plurality of polypeptides the presence of the molecule so as to encapsulate the molecule in the polymer.

44. The method as claimed in claim 43, wherein at least one of said polypeptides comprises a target vector.

45. A method of generating a variant comprising:

obtaining a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency, and fragments comprising at least 30 consecutive nucleotides of any of the foregoing sequences; and

modifying said sequence by one or more steps selected from the group consisting of modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, and adding one or more nucleotides to said sequence.

46. The method of claim 45, wherein the modifications are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis and any combination thereof.

47. The method of claim 46, wherein the modifications are introduced by error-prone PCR.

48. The method of claim 46, wherein the modifications are introduced by shuffling.

49. The method of claim 46, wherein the modifications are introduced by oligonucleotide-directed mutagenesis.

50. The method of claim 46, wherein the modifications are introduced by assembly PCR.

51. The method of claim 46, wherein the modifications are introduced by sexual PCR mutagenesis.

52. The method of claim 46, whcrein the modifications are introduced by in vivo mutagenesis.

53. The method of claim 46, wherein the modifications are introduced by cassette mutagenesis.

54. The method of claim 46, wherein the modifications are introduced by recursive ensemble mutagenesis.

55. The method of claim 46, wherein the modifications are introduced by exponential ensemble mutagenesis.

56. The method of claim 46, wherein the modifications are introduced by site-specific mutagenesis.

57. The method of claim 46, wherein the modifications are introduced by gene reassembly.

58. The method of claim 46, wherein the modifications are introduced by gene site saturated mutagenesis.

59. The method of claim 46, wherein at least one modification is made to a codon of the polynucleotide.

60. An assay for identifying functional polypeptide fragments or variants encoded by fragments of SEQ ID NOS: 1, 3, 5, 7, and 9, and sequences having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, which retain at least one property of the polypeptides of SEQ ID NOS: 2, 4, 6, 8, and 10, and sequences having at least about 50% homology to SEQ ID NOS: 2, 4, 6, 8 and 10, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, said assay comprising the steps of:

providing a solution of a plurality of polypeptides having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, and 10, and sequences having at least about 50% homology to SEQ ID NOS: 2, 4, 6, 8 and 10 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, polypeptide fragments or variants encoded by SEQ ID NOS: 1, 3, 5, 7, and 9, sequences having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and sequences complementary to any of the foregoing sequences, in a solution containing a template molecule and alkaline earth metal ion; and

detecting a presence of a polymer in the solution.

61. An assay as claimed in claim 60, wherein said step of detecting the presence of a polymer in the solution is carried out by analyzing the solution using a method selected from HPLC, GPC and light scattering.

62. A polypeptide comprising:

a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, sequences having at least 50% homology to a sequence selected from SEQ ID NOS: 2, 4, 6, 8, and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection; and

at least one functional group selected from the group consisting of an antibody, an oligosaccharide, a polynucleotide, and a polyethylene glycol.

63. The polypeptide as claimed in claim 62, wherein the at least one functional group comprises a polynucleotide.

64. The polypeptide as claimed in claim 62, wherein the side group comprises a polyethylene glycol.

65. The polypeptide as claimed in claim 62, wherein the at least one functional group comprises an oligosaccharide.

66. The polypeptide as claimed in claim 62, wherein the side group comprises an antibody.

67. A polypeptide comprising:

an amino acid sequence encoded by a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and

sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency., and

at least one functional group selected from the group consisting of an antibody, an oligosaccharide, a polynucleotide, and a polyethylene glycol.

68. The polypeptide as claimed in claim 67, wherein the at least one functional group comprises a polynucleotide.

69. The polypeptide as claimed in claim 67, wherein the at least one functional group comprises a polyethylene glycol.

70. The polypeptide as claimed in claim 67, wherein the at least one functional group comprises an oligosaccharide.

71. The polypeptide as claimed in claim 67, wherein the at least one functional group comprises an antibody.

72. A nucleic acid probe comprising an oligonucleotide from about 10 to 50 nucleotides in length and having a segment of at least 10 contiguous nucleotides that is at least 50% complementary to a nucleic acid target region of the nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1,3, 5, 7 and 9, and which hybridizes to the nucleic acid target region under moderate to highly stringent conditions to form a detectable target:probe duplex.

73. The probe of claim 72, wherein the oligonucleotide is DNA.

74. The probe of claim 73, which is at least 60% complementary to the nucleic acid target region.

75. The probe of claim 72, which is at least 70% complementary to the nucleic acid target region.

76. The probe of claim 72, which is at least 80% complementary to the nucleic acid target region.

77. The probe of claim 72, which is at least 90% complementary to the nucleic acid target region.

78. The probe of claim 72, which is fully complementary to the nucleic acid target region.

79. The probe of claim 72, wherein the oligonucleotide is 15-50 bases in length.

80. The probe of claim 72, wherein the probe further comprises a detectable isotopic label.

81. The probe of claim 72, wherein the probe further comprises a detectable non-isotopic label selected from the group consisting of a fluorescent molecule, a chemiluminescent molecule, an enzyme, a cofactor, an enzyme substrate, and a hapten.

82. A nucleic acid probe comprising an oligonucleotide from about 15 to 50 nucleotides in length and having a segment of at least 15 contiguous nucleotides that is at least 90% complementary to a nucleic acid target region of the nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, and

which hybridizes to the nucleic acid target region under moderate to highly stringent conditions to form a detectable target:probe duplex.

83. A nucleic acid probe as claimed in claim 82, wherein the oligonucleotide is at least 95% complementary to a nucleic acid target region of the nucleic acid sequence.

84. A nucleic acid probe as claimed in claim 82, wherein the oligonucleotide is at least 97% complementary to a nucleic acid target region of the nucleic acid sequence.

85. A separation agent comprising a polymer made by self-assembly of a plurality of polypeptides has at least 50% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

86. The separation agent as claimed in claim 85, wherein each of the plurality of polypeptides has at least 60% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

87. The separation agent as claimed in claim 85, wherein each of the plurality of polypeptides has at least 70% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

88. The separation agent as claimed in claim 85, wherein each of the plurality of polypeptides has at least 80% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

89. The separation agent as claimed in claim 85, wherein each of the plurality of polypeptides has at least 90% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

90. The separation agent as claimed in claim 85, wherein each of the plurality of polypeptides is a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

91. A method of isolating a chiral compound from a mixture comprising the steps of:

providing a polymeric separation agent as claimed in claim 85; and

eluting the mixture containing the chiral compound through the resin to achieve a separation of the chiral compound from rest material in the mixture.

92. A fiber comprising a polymer made by self-assembly of a plurality of polypeptides.

93. The fiber as claimed in claim 92, wherein each of the plurality of polypeptides has at least 50% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

94. A lubricant comprising:

a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has at least 50% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

95. A coating composition comprising a a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has at least 50% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

96. A biochip comprising a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has at least 50% homology

to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

97. A nanomechanical component comprising a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has at least 50% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

98. An optical switch comprising a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has at least 60% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

99. An optical waveguidecomprising a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has at least 50% homology to a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

100. A computer readable medium having stored thereon a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency.

101. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency.

102. The computer system of claim 101, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.

103. The computer system of claim 101, wherein the sequence comparison algorithm comprises a computer program which indicates polymorphisms.

104. The computer system of claim 101, further comprising an identifier which identifies one or more features in said sequence.

105. A method for comparing a first sequence to a second sequence comprising the steps of:

reading the first sequence and the second sequence through use of a computer program which compares sequences; and

determining differences between the first sequence and the second sequence with the computer program,

wherein said first sequence is a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50%

homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency.

106. The method of claim 105, wherein the step of determining differences between the first sequence and the second sequence further comprises the step of identifying polymorphisms.

107. A method for identifying a feature in a particular sequence comprising the steps of:

reading the particular sequence using a computer program which identifies one or more features in a sequence; and

identifying one or more features in the particular sequence with the computer program,

wherein the particular sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ lD NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency.

108. A protein preparation comprising a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, sequences having at least about 50% homology to a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm, and sequences having at least 10 consecutive amino acid residues of a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

109. An expression vector capable of replicating in a host cell comprising a polynucleotide having a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency.

110. An expression vector as claimed in claim 109, wherein the vector is selected from the group consisting of viral vectors, plasmid vectors, phage vectors, phagemid vectors, cosmids, fosmids, bacteriophages, artificial chromosomes, adenovirus vectors, retroviral vectors, and adeno-associated viral vectors.

111. A host cell comprising an expression vector as claimed in claim 109.

112. A host cell as claimed in claim 111, whereint the host is selected from the group consisting of prokaryotes, eukaryotes, funguses, yeasts, plants and metabolically rich hosts.